

ALIGNMENT

LOCUS AX076272 6995 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 1 from Patent WO0104325.
ACCESSION AX076272
VERSION AX076272.1 GI:12710897
KEYWORDS .
SOURCE Corynebacterium glutamicum.
ORGANISM Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
REFERENCE 1 (bases 1 to 6995)
AUTHORS Dunican, L.K., Stapleton, C., Burke, K. and Moeckel, B.
TITLE Nucleotide sequences for the tal gene
JOURNAL Patent: WO 0104325-A 1 18-JAN-2001;
Degussa-Huels Aktiengesellschaft (DE) ; National University of
Ireland (IE)

Query Match 100.0%; Score 828; DB 6; Length 6995;
Best Local Similarity 100.0%; Pred. No. 1.3e-196;
Matches 828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGAGCTCGCCACATGGATCCAGATTGGCTACCAGCACGCACATCCGGCTTGTCC 60
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Db 6093 GAGGAGCTCGCCACATGGATCCAGATTGGCTACCAGCACGCACATCCGGCTTGTCC 6152
Qy 61 AGCGTCAAGCTGGAAACCGTCTAAGGAGAAATACAACACTATGGTGTAGTACGCGC 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6153 AGCGTCAAGCTGGAAACCGTCTAAGGAGAAATACAACACTATGGTGTAGTACGCGC 6212
Qy 121 ACGCGATACTGAAGATTGGTGCACAGGCTGCCTCAAATTCAATTGAGGTTGTTGAAGC 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6213 ACGCGATACTGAAGATTGGTGCACAGGCTGCCTCAAATTCAATTGAGGTTGTTGAAGC 6272
Qy 181 AGCAACTGCCAATAATGGCACCGCACAGGTAGTGCTCACCGTGGTGGCGCCGGCATCAA 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6273 AGCAACTGCCAATAATGGCACCGCACAGGTAGTGCTCACCGTGGTGGCGCCGGCATCAA 6332
Qy 241 GTTGCTGGAAAAGCTCAGCGTTGATGCGGCTGACCTGCCTGGGATCGCATTGATGTGTT 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6333 GTTGCTGGAAAAGCTCAGCGTTGATGCGGCTGACCTGCCTGGGATCGCATTGATGTGTT 6392
Qy 301 CTTCGCGATGAGCGCAATGTCCCTGTCAGTGATTCTGAGTCCAATGAGGCCAGGCTCG 360
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Db 6393 CTTCGCGATGAGCGCAATGTCCCTGTCAGTGATTCTGAGTCCAATGAGGCCAGGCTCG 6452
Qy 361 TGAGGCACTGTTGTCAGGGTTCTATCCCTGAAGCCAACATTACCGGATATGGTCTCGG 420
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Db 6453 TGAGGCACTGTTGTCAGGGTTCTATCCCTGAAGCCAACATTACCGGATATGGTCTCGG 6512
Qy 421 CGACGTAGATCTGAGAGGCAGGCCGCGCTTACGAAGCTGTGGATGAATTGCGACC 480
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Db 6513 CGACGTAGATCTGAGAGGCAGGCCGCGCTTACGAAGCTGTGGATGAATTGCGACC 6572
Qy 481 AACGGCTTGATCTCACCTGCTCGGCATGGTGGCGAAGGCCATATCAACTCCCTGTT 540
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Db 6573 AACGGCTTGATCTCACCTGCTCGGCATGGTGGCGAAGGCCATATCAACTCCCTGTT 6632

Qy 541 CCCTCACACCGATGCAGTCAGGAATCCTCCGAAAGGTATCGCGTGTGATTCCCC 600
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Db 6633 CCCTCACACCGATGCAGTCAGGAATCCTCCGAAAGGTATCGCGTGTGATTCCCC 6692
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Qy 601 TAAGCCTCCTTCAGAGCGTGCAACTCTAACCTTCCTGCGGTTCACTCCGCAAAGCGCGT 660
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Db 6693 TAAGCCTCCTTCAGAGCGTGCAACTCTAACCTTCCTGCGGTTCACTCCGCAAAGCGCGT 6752
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Qy 661 GTGGTTGCTGGTTCTGGTGC GGAGAAGGCTGAGGCAGCTGCGCGATCGTCAACGGTGA 720
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Db 6753 GTGGTTGCTGGTTCTGGTGC GGAGAAGGCTGAGGCAGCTGCGCGATCGTCAACGGTGA 6812
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Qy 721 GCCTGCTGTTGAGTGGCCTGCTGCTGGAGCTACCGGATCTGAGGAAACGGTATTGTTCTT 780
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Db 6813 GCCTGCTGTTGAGTGGCCTGCTGCTGGAGCTACCGGATCTGAGGAAACGGTATTGTTCTT 6872
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Qy 781 GGCTGATGATGCTGCAGGAAATCTCTAACAGCAGCGCCAGCTCTAACAAAG 828
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Db 6873 GGCTGATGATGCTGCAGGAAATCTCTAACAGCAGCGCCAGCTCTAACAAAG 6920